

II. REMARKS

Upon entry of the present amendment, claims 1 to 11, 29 to 59, 66 to 70, and 74, 75, and 80 to 86 will be pending.

Applicants and Applicants' representative gratefully acknowledge the helpful comments and clarification of the Restriction Requirement by the Examiner in a telephone conference held May 5, 2003.

A. Regarding the Amendments

Pursuant to the Restriction Requirement, claims 12 to 28, 60 to 65, 71 to 73, and 76 to 79 are cancelled herein without disclaimer, and without prejudice to Applicants' pursuing prosecution of subject matter encompassed within one or more of the cancelled claims in an application claiming the benefit of priority of the subject application.

Claim 59 has been amended to correct the dependency from claim 58. The amendment is supported by a review of the SEQ ID NOS: recited in claims 58 and 59, wherein the SEQ ID NOS: recited in claim 59 are further limiting of those in claim 58. More specifically, the SEQ ID NOS: recited in claim 59 encompass only the regulatory element sequences recited in claim 58 (see, also, Table 2). Claim 59 also has been amended to delete a duplication of a comma. As such, it is submitted that the amendments merely address an informality and correct typographical errors, and do not add new matter.

New claims 80 to 86 have been added. New claims 80 to 86 are supported, for example, by paragraphs 9 and 10 (pages 3-4), paragraph 49 (page 28), and paragraph 51 (page 29.) It is noted that new claims 80 to 86 are based on the requirement to elect a single nucleotide sequence for examination, including fragments of the sequence. As discussed below, Applicants elect SEQ ID NO:1034 for examination. Applicants point out that SEQ ID NO:3729 (see new claim 81) comprises

the upstream genomic nucleotide sequence of SEQ ID NO:1034, including the stress responsive regulatory element (see Table 2; see, also SEQ ID NOS:1034 and 3729, attached hereto as Exhibits A and B, respectively, and GenBank Acc. No. AY056214, attached as Exhibit C.; wherein nucleotides 1 to 102 of GenBank Acc. No. AY056214 correspond to nucleotides 1576 to 1677 of SEQ ID NO:3729, and nucleotides 103 to 1172 correspond to nucleotides 1 to 1071 of SEQ ID NO:1034). As such, SEQ ID NO:3729 comprises the stress responsive regulatory element of elected SEQ ID NO:1034.

B. Regarding the Restriction Requirement

Applicants elect the claims of Group I, claims 1 to 11, 29 to 59, 66 to 70, 74 and 75 for examination.

It also is requested that ONE nucleotide sequence be selected for examination, and noted that the selected sequence can include, e.g., subsequences. Applicants select SEQ ID NO:1034. As discussed above, it is noted that SEQ ID NO:3729 comprises the upstream regulatory sequence for elected SEQ ID NO:1034. As such, it is respectfully requested that SEQ ID NO:3729 also be examined with elected SEQ ID NO:1034.

It also is stated in the Office Action that claims, including the claims elected herein, recite different combinations of nucleotide sequences, and requested that ONE combination of sequences be selected. Applicants select the combination of sequences that are regulated in response to Cold Stress, as set forth, e.g., in claim 2. It is noted that elected SEQ ID NO:1034 is included among the polynucleotides recited in claim 2. As discussed with the Examiner, it is further noted that claim 1 (and claim 2) can be practiced using only SEQ ID NO:1034, as well as using combinations of sequences including SEQ ID NO:1034.

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Filed: August 24, 2001
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PATENT
Attorney Docket No.: SCRIP1300-3

No additional fee beyond that enclosed herewith for the one month extension of time is deemed necessary in connection with the filing of this Response. However, if any fee is required, the Commissioner is authorized to charge any fee (or credit any overpayment) to Deposit Acct. No. 50-1355.

The Examiner is invited to contact Applicants' undersigned representative if there are any questions relating to this application.

Respectfully submitted,

Dated: May 14, 2003



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4365 Executive Drive, Suite 1100
San Diego, CA 92121-2133

Encl.: Exhibits A, B and C

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PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

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☐ 1: AY056214. Arabidopsis thali...[gi:15810350]

Links

LOCUS AY056214 1660 bp mRNA linear PLN 18-SEP-2002

DEFINITION Arabidopsis thaliana putative PCF2 DNA binding protein (At2g45680) mRNA, complete cds.

ACCESSION AY056214

VERSION AY056214.1 GI:15810350

KEYWORDS FLI_CDNA.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 1660)

AUTHORS Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

TITLE Arabidopsis Full Length cDNA Clones

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1660)

AUTHORS Yamada,K., Banh,J., Banno,F., Dale,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Tracy,S.E., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

TITLE Direct Submission

JOURNAL Submitted (12-SEP-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

COMMENT RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Banh,J., Banno,F., Dale,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tracy,S.E., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

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